GPPCTCKTILARAVAHHTDCTFIRVSGSELVOKYIGEGSRAVRELEVAAREHAPSILENDELDSIGSARAESGTCNCDSEVORTMLEILINOLDGFEASNK 264 8 164 GPFCTCACTLLARAVAHHIDCTCTRVSCAELVOKYICECSRAVRELEVAAREHAPSIIEMDEIDSIGSTRVE-GSG3CDSEVORTMIELLNOLDGFETSRN 287 GPPGICATILIARAVAHHIDCIFIRVSGSELVÇKFIGEGARMYRELFVMAREHAPSIIFMDEIDSIGSSRLEGGSG-GSSEVÇRÇMIELLINQIDGFEATKN 288 GPPGICATILARAVAHHIDCIFIRVSGSELVQKFIGEGARAVRELFVAAREHAPSIIFADEIDSIGSSRLEGGSG-GOSEVQRIMLEILNQIDGFEAIRN 288 GPPGICATILARAVAHHTDCTFIRVSGSELVOKFICEGRARAVRELFVARREHAPSIIFNDEIDSIGSSRLEGGSG-CEDSEVORIMLEILNQIDGFEATRN 288 GPPGICATILLARAVAHHIDCIFIRVSGSELVOKYIGEGSRAVRELFVAAREHAPSIIFVDEIDSIGSARVESGSGNODSEVORIMIELLINOLDGFEASNAK 300 HPEGKYVVDIDKSIDITKTTPSTRVALRNDSYMLHLILPSKVDPLVNLMKVEKVPDSTYDMIGGLDQQIKELKEVIELPIKHPELFESIGLAQPKGVILY HPECKYVVDIDKNIDITKITPSTRVALRNDSYVLHIVLPSKVDPIVNIMKVEKVPDSTYDMIGGIDQQIKEIKEVIEIPIKHPEIFESIGIAQPKGVILIX sel.pk0023.b5 cs1.pk0051.b7 138810 254219 P47210 X66400

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IKVIMATNRIDIIDSALIRPGRIDRKIEFPPPNEEARIDIIKIHSRKMUIRGINURKIAEIMPGASGAEVKGVOTEAGAYALRERRYHVIQEDFEMAVA 388 IKVIMATNRIDIIDSALIRPGRIDRKIEFPPPNEEARIDIIKIHSRKMUIRGINURKIAEIMPGASGAEVKGVOTEAGAYALRERRYHVIQEDFEMAVA 388 IKVIMATNRIDIIDPALIRPGRIDRKIEFPPPSVAARAEIIRIIKIHSRKMUIRGINURKIAEIMPGASGAEVKGVOTEAGAYALRERRYHVIQEDFEMAVA 388 IKVIMATNRIDIIDQALIRPGRIDRKIEFPPPSVAARAEIIRIHSRKMUIRGINIKKIAEKMASCGADVKGVOTEAGAYALRERRYHVIQEDFEMAVA 389 IKVIMATNRIDIIDQALIRPGRIDRKIEFPPPSVAARAEIIRIHSRRMUMRGIDIKKIAEKMASASGAEIKAVOTEAGAFALRERRYHVIQEDFEMAVA 400 IKVIMATNRIDIIDQALIRPGRIDRKIEFPNENEDSRFDIIKIHSRRMUMRGIDIKKIAEKMASASGAEIKAVOTEAGAFALRERRYHVIQEDFEMAVA 384	KVAZKOSEKNAKSIRKCIMK KVAZKOSEKNAKSIRKCIMK KVAZKOSEKNAKSIRKCIMK KVAZKOSEKNAKSIRKCIMK KVAKKOTEKNAKSIRKCIMK KVAKKOTEKNAKSIRKCIMK KVAKKOTEKNAKSIRKCIMK 382
254219	254219
P47210	P47210
138810	L38810
X66400	X66400
Se1.pk0023.b5	Sel.pk0023.b5
CS1.pk0051.b7	CSl.pk0051.b7



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## FIGURE 2

1 2 3 4	MATVAMDISKPTPAASGDEAAAAAKGRSGGGEGLRQYYLQHIHDLQLQIRQKTHNLNRL MALVGVELKHAAEGVPEANCSAKPTKQGEGLRHYYSLNIHEHQLLLRQKTHNLNRL MALDGPEQMELEEGKAGSGLRQYYLSKIEELQLIVNDKSQNLRRL MATVAMDISKPTPVASGDEAAAAAKGRSGGGGEGLRQYYLQHIHDLQLQIRHKTHNLNRL
1 2 3 4	EAQRNDLNSRVRMLREELQLLQEPGSYVGEVVKVMGKSKVLVKVHPEGKYVVDIDKSIDI EAQRNDLNSRVRMLREELQLLQEPGSYVGEVVKVMGKNKVLVKVHPEGKYVVDIDKNIDI QAQRNELNAKVRLLREELQLLQEQGSYVGEVVRAMDKKKVLVKVHPEGKFVVDVDKNIDI EAQRNDLNSRVRMLREDXXLLXEPGSYVGXVVKAWGNQRFWVKVNPEGKXXVDIN
1 2 3 4	TKITPSTRVALRNDSYMLHLILPSKVDPLVNLMKVEKVPDSTYDMIGGLDQQIKEIKEVI TKITPSTRVALRNDSYVLHLVLPSKVDPLVNLMKVEKVPDSTYDMIGGLDQQIKEIKEVI NDVTPNCRVALRNDSYTLHKILPNKVDPLVSLMMVEKVPDSTYEMIGGLDKQIKEIKEVI
1 2 3 4	ELPIKHPELFESLGIAQPKGVLLYGPPGTGKTLLARAVAHHTDCTFIRVSGSELVQKYIG ELPIKHPELFESLGIAQPKGVLLYGPPGTGKTLLARAVAHHTDCTFIRVSGSELVQKYIG ELPVKHPELFEALGIAQPKGVLLYGPPGTGKTLLARAVAHHTDCTFIRVSGSELVQKFIG
1 2 3 4	EGSRMVRELFVMAREHAPSIIFMDEIDSIGSARMESGTGNGDSEVQRTMLELLNQLDGFE EGSRMVRELFVMAREHAPSIIFMDEIDSIGSARMESGSGNGDSEVQRTMLELLNQLDGFE EGARMVRELFVMAREHAPSIIFMDEIDSIGSSRLEGGSG.GDSEVQRTMLELLNQLDGFE
1 2 3 4	ASNKIKVLMATNRIDILDQALLRPGRIDRKIEFPNPNEDSRFDILKIHSRKMNLMRGIDL ASNKIKVLMATNRIDILDQALLRPGRIDRKIEFPTPNEESRLDILKIHSRRMNLMRGIDL ATKNIKVIMATNRIDILDSALLRPGRIDRKIEFPPPNEEARLDILKIHSRKMNLTRGINL
1 2 3 4	KKIAEKMNGASGAELKAVCTEAGMFALRERRVHVTQEDFEMAVAKVMKKDTEKNMSLRKL KKIAEKMNGASGAELKAVCTEAGMFALRERRVHVTQEDFEMAVAKVMKKETEKNMSLRKL RKIAELMPGASGAEVKGVCTEAGMYALRERRVHVTQEDFEMAVAKVMQKDSEKNMSIKKL
1 2 3 4	WK WK WK